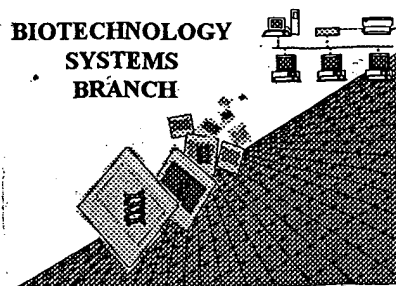


0590

0280
6400BIOTECHNOLOGY
SYSTEMS
BRANCH**RAW SEQUENCE LISTING**
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/024,036
 Source: O/PZ
 Date Processed by STIC: 1/15/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
 Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
 Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/024,036

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

OIEP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:40

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01152002\J024036.raw

4 <110> APPLICANT: Bandaru, Rajasekhar
6 <120> TITLE OF INVENTION: 68730 and 69112, Protein Kinase
7 Molecules and Uses Therefor
10 <130> FILE REFERENCE: MPI2000-521P1R(M)
12 <140> CURRENT APPLICATION NUMBER: US/10/024,036
12 <141> CURRENT FILING DATE: 2001-12-17
12 <150> PRIOR APPLICATION NUMBER: 60/258222
13 <151> PRIOR FILING DATE: 2000-12-22
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1772
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
24 <220> FEATURE:
25 <221> NAME/KEY: 5'UTR
26 <222> LOCATION: (1)...(168)
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (9)...(1242)
31 <221> NAME/KEY: 3'UTR
32 <222> LOCATION: (1243)...(1772)
34 <400> SEQUENCE: 1
W--> 35 ~~monnancg~~ cgg cgg cgt gcg cac gag cga aag agg aaa ctg cag agg agg 50
36 Arg Arg Arg Ala His Glu Arg Lys Arg Lys Leu Gln Arg Arg
37 1 5 10
39 aag ctg cgc cgc agc ccg agc cgc ccg gca tcc ccg ccg cct ctg cgc 98
40 Lys Leu Arg Arg Ser Pro Ser Arg Pro Ala Ser Pro Pro Pro Leu Arg
41 15 20 25 30
43 ccg cgc cgc gcc ccc gcc gcc ccc tcc cca gcg cgc ccc cgg ccg ctc 146
44 Pro Arg Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu
45 35 40 45
47 ctc cgc gcc gcg ctc gtc gcc cat gcc ccg gga gaa cgg cga gag cag 194
48 Leu Arg Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln
49 50 55 60
51 ctc ctc ctg gaa aaa gca agc tga aga cat caa gaa gat ctt cga gtt 242
52 Leu Leu Leu Glu Lys Ala Ser * Arg His Gln Glu Asp Leu Arg Val
53 65 70 75
55 caa aga gac cct cgg aac cgg gcc ctt ttc cga agt ggt ttt agc tga 290
56 Gln Arg Asp Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser *
57 80 85 90
59 aga gaa gcc aac tgg caa gct ctt tgc tgt gaa gtg tat ccc taa gaa 338
60 Arg Glu Gly Asn Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro * Glu
61 95 100 105
63 gcc gct gaa ggg caa gga aag cag cat aga gaa tga gat agc cgt cct 386
64 Gly Ala Glu Gly Gln Gly Lys Gln His Arg Glu * Asp Ser Arg Pro
65 110 115 120
67 gag aaa gat taa gca tga aaa tat tgt tgc cct gga aga cat tta tga 434

see p. 5, too
**Does Not Comply
Corrected Diskette Needed**

see item 9 on Error Summary Sheet

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
 TIME: 18:18:40

Input Set : A:\seq list.txt
 Output Set: N:\CRF3\01152002\J024036.raw

```

68 Glu Lys Asp * Ala * Lys Tyr Cys Cys Pro Gly Arg His Leu *
69 125 130 135
71 aag ccc aaa tca cct gta ctt ggt cat gca gct ggt gtc cgg tgg aga 482
72 Lys Pro Lys Ser Pro Val Leu Gly His Ala Ala Gly Val Arg Trp Arg
73 140 145 150
75 gct gtt tga ccg gat agt gga gaa ggg gtt tta tac aga gaa gga tgc 530
76 Ala Val * Pro Asp Ser Gly Glu Gly Val Leu Tyr Arg Glu Gly Cys
77 155 160 165
79 cag cac tct gat ccg cca agt ctt gga cgc cgt gta cta tct cca cag 578
80 Gln His Ser Asp Pro Pro Ser Leu Gly Arg Arg Val Leu Ser Pro Gln
81 170 175 180
83 aat ggg cat cgt cca cag aga cct caa gcc cga aaa tct ctt gta cta 626
84 Asn Gly His Arg Pro Gln Arg Pro Gln Ala Arg Lys Ser Leu Val Leu
85 185 190 195
87 cag tca aga tga gga gtc caa aat aat gat cag tga ctt tgg att gtc 674
88 Gln Ser Arg * Gly Val Gln Asn Asn Asp Gln * Leu Trp Ile Val
89 200 205 210
91 aaa aat gga ggg caa agg aga tgt gat gtc cac tgc ctg tgg aac tcc 722
92 Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys Leu Trp Asn Ser
93 215 220 225
95 agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cag caa agc 770
96 Arg Leu Cys Arg Ser * Ser Pro Arg Pro Glu Thr Leu Gln Gln Ser
97 230 235 240
99 cgt tga ctg ctg gtc cat ccg agt gat tgc cta cat ctt gct ctg ccg 818
100 Arg * Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala Leu Arg
101 245 250 255
103 cta ccc tcc ttt tta tga tga aaa tga ctc caa gct ctt tga gca gat 866
104 Leu Pro Ser Phe Leu * * Lys * Leu Gln Ala Leu * Ala Asp
105 260 265 270
107 cct caa ggc gga ata tga gtt tga ctc tcc cta ctg gga tga cat ctc 914
108 Pro Gln Gly Gly Ile * Val * Leu Ser Leu Leu Gly * His Leu
109 275 280
111 cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga ccc gaa 962
112 Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu
113 285 290 295
115 taa aag ata cac gtg tga gca ggc agc tcg gca ccc atg gat cgc tgg 1010
116 * Lys Ile His Val * Ala Gly Ser Ser Ala Pro Met Asp Arg Trp
117 300 305 310
119 tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat 1058
120 * His Ser Pro Gln Gln Lys His Pro Arg Val Arg Gln Arg Pro Asp
121 315 320 325
123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac 1106
124 Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile * Cys His
125 330 335 340
127 ggc cgt cgt gag aca tat gag aaa act aca cct ccg cag cag cct gga 1154
128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly
129 345 350 355
131 cag ttc aaa tgc aag tgt ttc gag cag cct cag ttt ggc cag cca aaa 1202
132 Gln Phe Lys Cys Lys Cys Phe Glu Gln Pro Gln Phe Gly Gln Pro Lys

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002

TIME: 18:18:40

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01152002\J024036.raw

```

133 360                               375
135 aga ctg tgc gta tgt agc aaa acc aga atc cct cag ctg a cactgaagac 1252
136 Arg Leu Cys Val Cys Ser Lys Thr Arg Ile Pro Gln Leu
137                               380       385
139 gagcctgggg tggagaggag ggagccggca tctgccgagc acctcctgtt tgccaggcgc 1312
140 tttctatact taatcccatg tcatgcgacc ctaggacttt ttttaacatg taatcactgg 1372
141 gccgggtgca gtggctcacg cctgtaatcc caacactttg ggaggtctgag gcaggaggac 1432
142 tgtttgagtt caggagtttt aagaccagcc tgaccaacat ggtgaaaccc catctctact 1492
143 aaaatataaa aattagccgg gtgtgggtggc gagcacctgt aatgtcagct acttgggagg 1552
144 ctgaggcagg agaatcactt gaaccaggga agcggagggt gcaatgagct gagatcacac 1612
145 cactgcactc cagcctgggt gacagattga gactccctct caaaaaaaaaa agggaaatca 1672
146 ttgaacactc gtggaaccct aggtattgca tattccattt acggtttggg aatccagggc 1732
147 tcaagtcttc gcaggggtac cgagctcgag atcgtaatca 1772
149 <210> SEQ ID NO: 2
150 <211> LENGTH: 388
151 <212> TYPE: PRT
152 <213> ORGANISM: Human
154 <400> SEQUENCE: 2
155 Arg Arg Arg Ala His Glu Arg Lys Arg Lys Leu Gln Arg Arg Lys Leu
156 1 5 10 15
157 Arg Arg Ser Pro Ser Arg Pro Ala Ser Pro Pro Pro Leu Arg Pro Arg
158 20 25 30
159 Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu Leu Arg
160 35 40 45
161 Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln Leu Leu
162 50 55 60
163 Leu Glu Lys Ala Ser Arg His Gln Glu Asp Leu Arg Val Gln Arg Asp
164 65 70 75 80
165 Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser Arg Glu Gly Asn
166 85 90 95
167 Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro Glu Gly Ala Glu Gly Gln
168 100 105 110
169 Gly Lys Gln His Arg Glu Asp Ser Arg Pro Glu Lys Asp Ala Lys Tyr
170 115 120 125
171 Cys Cys Pro Gly Arg His Leu Lys Pro Lys Ser Pro Val Leu Gly His
172 130 135 140
173 Ala Ala Gly Val Arg Trp Arg Ala Val Pro Asp Ser Gly Glu Gly Val
174 145 150 155 160
175 Leu Tyr Arg Glu Gly Cys Gln His Ser Asp Pro Pro Ser Leu Gly Arg
176 165 170 175
177 Arg Val Leu Ser Pro Gln Asn Gly His Arg Pro Gln Arg Pro Gln Ala
178 180 185 190
179 Arg Lys Ser Leu Val Leu Gln Ser Arg Gly Val Gln Asn Asn Asp Gln
180 195 200 205
181 Leu Trp Ile Val Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys
182 210 215 220
183 Leu Trp Asn Ser Arg Leu Cys Arg Ser Ser Pro Arg Pro Glu Thr Leu
184 225 230 235 240
185 Gln Gln Ser Arg Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:40

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01152002\J024036.raw

```

186                               245                250                255
187 Leu Arg Leu Pro Ser Phe Leu Lys Leu Gln Ala Leu Ala Asp Pro Gln
188                               260                265                270
189 Gly Gly Ile Val Leu Ser Leu Leu Gly His Leu Arg Leu Cys Lys Arg
190                               275                280                285
191 Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu Lys Ile His Val Ala
192                               290                295                300
193 Gly Ser Ser Ala Pro Met Asp Arg Trp His Ser Pro Gln Gln Lys His
194                               305                310                315
195 Pro Arg Val Arg Gln Arg Pro Asp Pro Glu Lys Leu Cys Gln Glu Gln
196                               320                325                330
197 Met Glu Thr Ser Ile Cys His Gly Arg Arg Glu Thr Tyr Glu Lys Thr
198                               335                340                345
199 Thr Pro Arg Gln Gln Pro Gly Gln Phe Lys Cys Lys Cys Phe Glu Gln
200                               350                355                360
201 Pro Gln Phe Gly Gln Pro Lys Arg Leu Cys Val Cys Ser Lys Thr Arg
202                               365                370                375
203 Ile Pro Gln Leu
204 385
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1074
209 <212> TYPE: DNA
210 <213> ORGANISM: Human
212 <400> SEQUENCE: 3

```

```

213 atggcccggg agaacggcga gagcagctcc tcctggaaaa agcaagctga agacatcaag 60
214 aagatcttcg agttcaaaga gacctcgga accggggcct tttccgaagt ggttttagct 120
215 gaagagaagg caactggcaa gctctttgct gtgaagtgtg tccctaagaa ggcgctgaag 180
216 ggcaaggaaa gcagcataga gaatgagata gccgtcctga gaaagattaa gcatgaaaat 240
217 attgttgccc tggaagacat ttatgaaagc ccaaatcacc tgtacttggg catgcagctg 300
218 gtgtccgggtg gagagctgtt tgaccggata gtggagaagg ggttttatac agagaaggat 360
219 gccagcactc tgatccgcca agtcttggac gccgtgtact atctccacag aatgggcatc 420
220 gtccacagag acctcaagcc cgaaaatctc ttgtactaca gtcaagatga ggagtccaaa 480
221 ataagatgca gtgacttttg attgtcaaaa atggagggca aaggagatgt gatgtccact 540
222 gcctgtggaa ctccaggcta tgtcgctcct gaagtcctcg cccagaaacc ttacagcaaa 600
223 gccgttgact gctggtccat cggagtgtatt gcctacatct tgctctgcgg ctacctcct 660
224 ttttatgatg aaaatgactc caagctcttt gagcagatcc tcaaggcgga atatgagttt 720
225 gactctccct actgggatga catctccgac tctgcaaaaag acttcattcg gaacctgatg 780
226 gagaaggacc cgaataaaaag atacacgtgt gagcaggcag ctcggcaccc atggatcgct 840
227 ggtgacacag ccctcaacaa aaacatccac gaggccgta ggcgccagat ccggaaaaaac 900
228 tttgccaaga gcaaatggag acaagcattt aatgccacgg ccgtcgtgag acatatgaga 960
229 aaactacacc tcggcagcag cctggacagt tcaaatgcaa gtgttttcgag cagcctcagt 1020
230 ttggccagcc aaaaagactg tgcgtatgta gcaaaaccag aatccctcag ctga 1074

```

```

232 <210> SEQ ID NO: 4
233 <211> LENGTH: 3579
234 <212> TYPE: DNA
235 <213> ORGANISM: Human
237 <220> FEATURE:
238 <221> NAME/KEY: 5'UTR
239 <222> LOCATION: (1)...(1212)

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002

TIME: 18:18:40

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01152002\J024036.raw

```

241 <221> NAME/KEY: CDS
242 <222> LOCATION: (1213)...(3159)
244 <221> NAME/KEY: 3'UTR
245 <222> LOCATION: (3160)...(3579)
247 <400> SEQUENCE: 4
248 aacagttctg tcacttggtc gacatttaac acatgtgagt tgtatgaatg cctaaaggcc 60
249 ataccatgct gcctgggaaa cagcaagaac tccatcagtg gcagagacta tcactattat 120
250 tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttgagg ggaaaaagta 180
251 cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg 240
252 gctgattttg gacttgcaaa gcatgtggtg agacctatat ttactgtgtg tgggacccca 300
253 acttacgtag ctcccgaaat tctttctgag aaaggttatg gactggaggt ggacatgtgg 360
254 gctgctggcg tgatcctcta tatcctgctg tgtggctttc ccccatcccg cagccctgag 420
255 agggaccagg acgagctctt taacatcatc cagctggggc actttgagtt cctccccctt 480
256 tactgggaca atatctctga tgctgctaaa gatctggtga gccggttgct ggtggtagac 540
257 cccaaaaagc gctacacagc tcatcagggt cttcagcacc cctggatcga aacagctggc 600
258 aagaccaata cagtgaacag acagaagcag gtgtcccccgc gcagcgaggg tcacttcccg 660
259 agccagcaca agagggttgt ggagcaggta tcatatcygc tgagggtcga agatgtgtct 720
260 cttaaagccc caaattccca ctcaacttct catagccatt atgactgatt tagctgaata 780
261 accttgggac agcaaggcct atgtgacccat tctctaaaaat atttaagctc gagaatcaca 840
262 gagcggaagc tgcaaggctc ctggctgcct gccagccgag ggaatctgga gaaaccattc 900
263 ctggggccgc gtggcccgct cgtgcccttg ttctgccctc ggaatggcct tcactcagca 960
264 catcctgaga acagccctct gaagcccagg gtctgaccgc tagtgaagct ggtgggcag 1020
265 cgcccccgaa agatcactct gctcctcaac aggcgatcag tgcagacggt cgagcagctc 1080
266 ttagctgaca tctcagaagc cttgggctct ccagatgga agaatagacc tgtgaggaaa 1140
267 ctgtttaacc tcaagggcag ggaaatcagg agcgtctctg atttcttcag ggaaggggat 1200
268 gctttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251
269 Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val
270 1 5 10
272 gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc 1299
273 Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
274 15 20 25
276 cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc 1347
277 Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
278 30 35 40 45
280 aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag 1395
281 Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
282 50 55 60
284 agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg 1443
285 Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
286 65 70 75
288 aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag 1491
289 Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
290 80 85 90
292 aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc 1539
293 Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
294 95 100 105
296 agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt 1587
297 Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu
298 110 115 120 125

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002

TIME: 18:18:41

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01152002\J024036.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10